

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/519,476
Source: PCT
Date Processed by STIC: 4-3-06

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 04/03/2006

PATENT APPLICATION: US/10/519,476

TIME: 08:20:00

Input Set : A:\793392_1.TXT

Output Set: N:\CRF4\04032006\J519476.raw

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4 <110> APPLICANT: GENOMINE INC.
5      KOREA RESEARCH INSTITUTE OF CHEMICAL TECHNOLOGY
7 <120> TITLE OF INVENTION: Novel polypeptide having function of 7-keto-8-
aminopelargonic
8      acid synthase of plant and method for inducing growth inhibition
9      and lethality by suppressing expression of the polypeptide
11 <130> FILE REFERENCE: OP03-1029
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/519,476
C--> 13 <141> CURRENT FILING DATE: 2004-12-30
13 <150> PRIOR APPLICATION NUMBER: KR 2002-38011
14 <151> PRIOR FILING DATE: 2002-07-02
16 <160> NUMBER OF SEQ ID NOS: 6
18 <170> SOFTWARE: KopatentIn 1.71
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 1410
22 <212> TYPE: DNA
23 <213> ORGANISM: Arabidopsis thaliana
25 <400> SEQUENCE: 1
26 atggcggatc attcgtggga taaaactgtg gaagaagcag tgaatgtgct tgaatccagg      60
28 caaattcttc gatctttgag gcccatattgc atgtctaggc aaaacgaaga agaaatagtg      120
30 aaaagcagag ccaatggagg agacgggtac gaggtgttcg acggtttgtg tcaatgggat      180
32 cggacttcag ttgaggtgtc tgtctcgatt cctacatttc agaaatggct tcacgatgaa      240
34 ccagcaacg gagaagagat ttttagtgga gatgcattag ctgagtgtag aaaagggaga      300
36 ttcaagaagc tgcttttggt ctctgggaat gattatttgg gtttgagctc acatcctaca      360
38 atatcaaacg ctgctgcaaa cgcagtcaaa gaatatggtg tgggacctaa gggttctgct      420
40 ttaatattgt gctataccac ttatcatcgt ttgcttgagt ctagtttggc gcaactgaag      480
42 aaaaaagagg attgtcttgt ttgtcctact gggtttgctg ccaatatggc tgcaatgggt      540
44 gcaattggaa gtgttgcttc tcttttggcc gctagcggga aacctctgaa gaatgaaaaa      600
46 gttgccatct tttctgatgc gctgaatcat gcatcaatta ttgatggtgt ccgtcttgct      660
48 gaacgacaag gaaatgttga agtttttggt tatcgacact gtgacatata aaattgcaaa      720
50 atgaagagga aggtcgtggt gactgatagc ttatttagta tggacggtga ctttgacca      780
52 atggaagagc tctctcagct tcggaagaag tatggcttcc ttctagttaa tgatgatgct      840
54 catggaacat ttgtctgtgg agaaaacggt ggtggcgtgg ctgaggaatt taactgtgaa      900
56 gctgatgtag atttatgtgt gggcactttg agtaaggcag cagggtgtca tggcggtttc      960
58 atagcttgca gcaaaaaatg gaagcaactg atacagtcga gaggtcgttc attcatattt      1020
60 tcaacagcaa tccctgtccc aatggctgca gctgcttatg cagcagttgt agtggcgagg      1080
62 aaggagatat ggagaagaaa ggcaatatgg gagagggtaa aagagttcaa ggaattatct      1140
64 ggagttgaca tctcaagccc cattatctca cttgtttagt ggaatcaaga gaaagccctc      1200
66 aaagcgagcc ggtatctatt aaaatcaggc ttccatgtaa tggcaatacg accgccaca      1260
68 gtgccacca attcttgtag gctaaggggtg aactgagtg cagcacatac cacagaagat      1320
70 gtgaagaaac tcatcactgc gctttcttct tgtttggact ttgacaacac agccactcac      1380
72 attccttctt ttctatttcc caaattataa
75 <210> SEQ ID NO: 2
76 <211> LENGTH: 469

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77 <212> TYPE: PRT
78 <213> ORGANISM: Arabidopsis thaliana
80 <400> SEQUENCE: 2
81 Met Ala Asp His Ser Trp Asp Lys Thr Val Glu Glu Ala Val Asn Val
82   1           5           10           15
84 Leu Glu Ser Arg Gln Ile Leu Arg Ser Leu Arg Pro Ile Cys Met Ser
85           20           25           30
87 Arg Gln Asn Glu Glu Glu Ile Val Lys Ser Arg Ala Asn Gly Gly Asp
88           35           40           45
90 Gly Tyr Glu Val Phe Asp Gly Leu Cys Gln Trp Asp Arg Thr Ser Val
91           50           55           60
93 Glu Val Ser Val Ser Ile Pro Thr Phe Gln Lys Trp Leu His Asp Glu
94   65           70           75           80
96 Pro Ser Asn Gly Glu Glu Ile Phe Ser Gly Asp Ala Leu Ala Glu Cys
97           85           90           95
99 Arg Lys Gly Arg Phe Lys Lys Leu Leu Phe Ser Gly Asn Asp Tyr
100           100           105           110
102 Leu Gly Leu Ser Ser His Pro Thr Ile Ser Asn Ala Ala Ala Asn Ala
103           115           120           125
105 Val Lys Glu Tyr Gly Met Gly Pro Lys Gly Ser Ala Leu Ile Cys Gly
106           130           135           140
108 Tyr Thr Thr Tyr His Arg Leu Leu Glu Ser Ser Leu Ala Gln Leu Lys
109 145           150           155           160
111 Lys Lys Glu Asp Cys Leu Val Cys Pro Thr Gly Phe Ala Ala Asn Met
112           165           170           175
114 Ala Ala Met Val Ala Ile Gly Ser Val Ala Ser Leu Leu Ala Ala Ser
115           180           185           190
117 Gly Lys Pro Leu Lys Asn Glu Lys Val Ala Ile Phe Ser Asp Ala Leu
118           195           200           205
120 Asn His Ala Ser Ile Ile Asp Gly Val Arg Leu Ala Glu Arg Gln Gly
121           210           215           220
123 Asn Val Glu Val Phe Val Tyr Arg His Cys Asp Ile Ser Asn Cys Lys
124 225           230           235           240
126 Met Lys Arg Lys Val Val Val Thr Asp Ser Leu Phe Ser Met Asp Gly
127           245           250           255
129 Asp Phe Ala Pro Met Glu Glu Leu Ser Gln Leu Arg Lys Lys Tyr Gly
130           260           265           270
132 Phe Leu Leu Val Ile Asp Asp Ala His Gly Thr Phe Val Cys Gly Glu
133           275           280           285
135 Asn Gly Gly Gly Val Ala Glu Glu Phe Asn Cys Glu Ala Asp Val Asp
136           290           295           300
138 Leu Cys Val Gly Thr Leu Ser Lys Ala Ala Gly Cys His Gly Gly Phe
139 305           310           315           320
141 Ile Ala Cys Ser Lys Lys Trp Lys Gln Leu Ile Gln Ser Arg Gly Arg
142           325           330           335
144 Ser Phe Ile Phe Ser Thr Ala Ile Pro Val Pro Met Ala Ala Ala
145           340           345           350
147 Tyr Ala Ala Val Val Val Ala Arg Lys Glu Ile Trp Arg Arg Lys Ala
148           355           360           365

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150 Ile Trp Glu Arg Val Lys Glu Phe Lys Glu Leu Ser Gly Val Asp Ile
151      370                      375                      380
153 Ser Ser Pro Ile Ile Ser Leu Val Val Gly Asn Gln Glu Lys Ala Leu
154 385                      390                      395                      400
156 Lys Ala Ser Arg Tyr Leu Leu Lys Ser Gly Phe His Val Met Ala Ile
157                      405                      410                      415
159 Arg Pro Pro Thr Val Pro Pro Asn Ser Cys Arg Leu Arg Val Thr Leu
160                      420                      425                      430
162 Ser Ala Ala His Thr Thr Glu Asp Val Lys Lys Leu Ile Thr Ala Leu
163                      435                      440                      445
165 Ser Ser Cys Leu Asp Phe Asp Asn Thr Ala Thr His Ile Pro Ser Phe
166      450                      455                      460
168 Leu Phe Pro Lys Leu
169 465
172 <210> SEQ ID NO: 3
173 <211> LENGTH: 28
174 <212> TYPE: DNA
175 <213> ORGANISM: Artificial Sequence
177 <220> FEATURE:
178 <223> OTHER INFORMATION: Forward primer for AtKAPAS gene
181 <400> SEQUENCE: 3
182 ggcggatcct tcgcccaaat cacaattc                                     28
185 <210> SEQ ID NO: 4
186 <211> LENGTH: 32
187 <212> TYPE: DNA
188 <213> ORGANISM: Artificial Sequence
190 <220> FEATURE:
191 <223> OTHER INFORMATION: Reverse primer for AtKAPAS gene
194 <400> SEQUENCE: 4
195 ggcaagcttt tcaactgacaa tatcagaaac aa                               32
198 <210> SEQ ID NO: 5
199 <211> LENGTH: 26
200 <212> TYPE: DNA
201 <213> ORGANISM: Artificial Sequence
203 <220> FEATURE:
204 <223> OTHER INFORMATION: Forward primer for AtKAPAS gene
207 <400> SEQUENCE: 5
208 gcagatcttc gcccaaatca caattc                                     26
211 <210> SEQ ID NO: 6
212 <211> LENGTH: 31
213 <212> TYPE: DNA
214 <213> ORGANISM: Artificial Sequence
216 <220> FEATURE:
217 <223> OTHER INFORMATION: Reverse primer for AtKAPAS gene
220 <400> SEQUENCE: 6
221 gcagatcttt cactgacaat atcagaaaca a                               31

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/519,476

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date